



09,883,118.

Cole  
\$

PATENT  
Customer No. 22,852  
Attorney Docket No. 6832.0017

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re U.S. Patent No.: 6,905,688 )  
)  
Inventors: )  
)  
Craig A. Rosen and William A. Haseltine )  
)  
Issue Date.: June 14, 2005 )  
)  
For: ALBUMIN FUSION PROTEINS )

**Certificate**  
**MAR 09 2006**  
**of Correction**

Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

03/08/2006 SZEWDIE1 00000067 6905688

01 FC:1011

100.00 OP

Sir:

**REQUEST FOR CERTIFICATE OF CORRECTION**

Pursuant to 35 U.S.C. §§ 254 and 255, and 37 C.F.R. §§ 1.322 and 1.323, this is a request for a Certificate of Correction in the above-identified patent. Some of the mistakes identified in the appended Form occurred through the fault of the Patent Office, as clearly disclosed by the records of the application which matured into this patent.

For example, the priority claims to Provisional Application Nos. 60/256,931, filed December 21, 2000; 60/199,384, filed April 25, 2000; and 60/229,358, filed April 12, 2000, were deleted in an Amendment filed June 3, 2004, and a Corrected Filing Receipt reflecting the change was mailed by the PTO on June 21, 2004. However, the issued patent was printed with the priority claims in the title page under item (60) and in the first paragraph of the specification.

03/08/2006 SZEWDIE1 00000067 6905688

01 FC:1011

100.00 OP

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Moreover, the issued patent reflects the original Sequence Listing filed rather than the Substitute Sequence Listing submitted on May 12, 2004. The Sequence Listing in the attached Certificate of Correction is identical to the Substitute Sequence Listing filed on May 12, 2004, and is also identical to the computer readable copy of the Substitute Sequence Listing also submitted on May 18, 2004. Thus, the correction contains no new matter.

Finally, the issued patent contains an error in the claims due to an Office mistake. The issued claims are based on an Examiner's Amendment mailed with a Notice of Allowance dated February 12, 2004. Claim 4 recited "in vivo biological activity" in the Examiner's Amendment but the patent issued as "in viva biological activity." The Certificate of Correction corrects this typographical error.

Other mistakes identified in the appended Form are of a clerical or typographical nature, or of minor character, and resulted from an error made in good faith by Patentees by failing to bring to the attention of the Examiner the clerical/typographical errors in the claims presented in the Examiner's Amendment of February 12, 2004.

A check in the amount of \$100 (the fee set forth in 37 C.F.R. § 1.20(a)) is attached. Should a check not be appended or should any additional fees be needed, authorization is hereby given to charge any fees due in connection with the filing of this request to Deposit Account No. 06-0916.

Two (2) copies of PTO Form 1050 are appended. The complete Certificate of Correction involves twenty-seven (27) pages. Issuance of the Certificate of Correction containing the correction is earnestly requested.

Please charge any required fees not included herewith to our deposit account

06-0916.

Respectfully submitted,

FINNEGAN, HENDERSON, FARABOW,  
GARRETT & DUNNER, L.L.P.

Dated: March 7, 2006

By: Charles E. Van Horn  
Charles E. Van Horn  
Reg. No. 40,266

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**UNITED STATES PATENT AND TRADEMARK OFFICE**  
**CERTIFICATE OF CORRECTION**

PATENT NO. 6,905,688  
APPLICATION NO.: 09/833,118  
ISSUE DATE: June 14, 2005  
INVENTOR(S): Craig A. Rosen et al.

It is hereby certified that an error or errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

In the Title Page

Under item (60) (Related U.S. Application Data) of the title page, delete the text beginning with "Provisional application No. 60/229,358" to and ending "provisional application No. 60/199,384, filed on Apr. 25, 2000."

In the Specification:

Col. 1, line 3, delete the text beginning with "This application" to and ending "in its entirety." in col. 1, line 8.

In the Claims:

Col. 292, lines 36-37, in claim 1(j), delete the text "wherein the brain derived neurotrophic factor protein or fragment thereof,".

Col. 292, line 57, in claim 4, "viva" should read --vivo--.

Col. 294, line 15, in claim 15, delete "any of".

Col. 294, line 17, in claim 16, delete "any of".

In the Sequence Listing:

Delete the Sequence Listing beginning in Col. 263, beginning with the text "<160> NUMBER OF SEQ ID NOS: 35" to and ending "<400> SEQUENCE: 35

Met	Pro	Thr	Trp	Ala	Trp	Trp	Leu	Phe	Leu	Val	Leu	Leu	Leu	Ala	Leu
1					5				10					15	

MAILING ADDRESS OF SENDER

U.S. Patent No. 6,905,688

Finnegan, Henderson, Farabow,  
Garrett & Dunner, L.L.P.  
901 New York Avenue, N.W.  
Washington, D.C. 20001-4413

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Trp Ala Pro Ala Arg Gly"  
20

in Col. 292 and insert the following Sequence Listing:

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<211> 23

<212> DNA

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<221> primer\_bind

<223> primer useful to clone human growth hormone cDNA

<400> 1

cccaagaatt cccttatcca ggc

23

<210> 2

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<223> primer useful to clone human growth hormone cDNA

<400> 2

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33

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with non-cohesive ends.

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16

<210> 4

<211> 17

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<213> Artificial Sequence

<220>

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with non-cohesive ends.

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Washington, D.C. 20001-4413

<400> 4  
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17

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<221> misc\_structure  
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<210> 6  
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<223> invertase leader sequence

<220>  
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Ile Ser Ala Asp Ala His Lys Ser  
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<210> 8  
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<212> DNA  
 <213> Artificial Sequence

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 <223> synthetic oligonucleotide used to join DNA  
 fragments with non-cohesive ends.

<400> 8  
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 <213> Artificial Sequence

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<210> 10  
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<220>  
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<400> 11  
 tgtggaagag cctcagaatt tattcccaac 30

<210> 12  
 <211> 31  
 <212> DNA

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<213> Artificial Sequence

<220>

<221> misc\_structure

<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

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<211> 47

<212> DNA

<213> Artificial Sequence

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<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

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<212> DNA

<213> Artificial Sequence

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<221> misc\_structure

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<210> 15

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<213> Artificial Sequence

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ac 62

<210> 16

<211> 63

<212> DNA

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<213> Artificial Sequence

<220>

<221> misc\_structure

<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

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<212> DNA

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gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag 96  
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln  
20 25 30

cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144  
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
35 40 45

ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa 192  
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys  
50 55 60

tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt 240  
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
65 70 75 80

cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct 288  
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
85 90 95

gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc 336  
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu  
100 105 110

ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat 384  
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
115 120 125

gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga 432  
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

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aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg	480		
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg			
145	150	155	160
tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc	528		
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala			
165	170	175	
tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg	576		
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser			
180	185	190	
tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa	624		
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu			
195	200	205	
aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc	672		
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro			
210	215	220	
aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa	720		
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys			
225	230	235	240
gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac	768		
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp			
245	250	255	
agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc	816		
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser			
260	265	270	
agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac	864		
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His			
275	280	285	
tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca	912		
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser			
290	295	300	
tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct	960		
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala			
305	310	315	320
gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga	1008		
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg			
325	330	335	
agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca	1056		
Arg His Pro Asp Tyr Ser Val Val Leu Leu Arg Leu Ala Lys Thr			
340	345	350	
tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa	1104		
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu			
355	360	365	

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tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct	1152
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro	
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cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag	1200
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu	
385 390 395 400	
tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc	1248
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro	
405 410 415	
caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa	1296
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys	
420 425 430	
gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt	1344
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys	
435 440 445	
gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat	1392
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His	
450 455 460	
gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc	1440
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser	
465 470 475 480	
ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca	1488
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr	
485 490 495	
tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat	1536
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp	
500 505 510	
ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca	1584
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala	
515 520 525	
ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg	1632
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu	
530 535 540	
aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag	1680
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys	
545 550 555 560	
gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt	1728
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val	
565 570 575	
gct gca agt caa gct gcc tta ggc tta taacatctac atttaaaagc atctcag	1782
Ala Ala Ser Gln Ala Ala Leu Gly Leu	
580 585	

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Washington, D.C. 20001-4413

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<213> Homo Sapiens

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      35             40             45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
      50             55             60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
      65             70             75             80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
      85             90             95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
      100            105            110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
      115            120            125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
      130            135            140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
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Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
      165            170            175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
      180            185            190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
      195            200            205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
      210            215            220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
      225            230            235            240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
      245            250            255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
      260            265            270

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Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His  
 275 280 285  
 Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser  
 290 295 300  
 Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala  
 305 310 315 320  
 Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg  
 325 330 335  
 Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr  
 340 345 350  
 Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu  
 355 360 365  
 Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro  
 370 375 380  
 Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu  
 385 390 395 400  
 Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro  
 405 410 415  
 Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys  
 420 425 430  
 Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys  
 435 440 445  
 Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His  
 450 455 460  
 Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser  
 465 470 475 480  
 Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr  
 485 490 495  
 Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp  
 500 505 510  
 Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala  
 515 520 525  
 Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu  
 530 535 540  
 Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys  
 545 550 555 560  
 Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val  
 565 570 575

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Ala Ala Ser Gln Ala Ala Leu Gly Leu  
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site in pPPC0006

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site in pPPC0006

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Garrett & Dunner, L.L.P.  
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Washington, D.C. 20001-4413

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<211> 60  
<212> DNA  
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<210> 25  
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<212> DNA  
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fusion protein in which the albumin moiety is N-terminal  
of the Therapeutic Protein

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<222> (18)  
<223> n equals a,t,g, or c

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<221> misc feature  
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<222> (20)

MAILING ADDRESS OF SENDER

U.S. Patent No. 6,905,688

Finnegan, Henderson, Farabow,  
Garrett & Dunner, L.L.P.  
901 New York Avenue, N.W.  
Washington, D.C. 20001-4413

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MAR 9 2006



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MAR 9 2000

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MAR 9 2000

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tctcccgga tctgaggtc acatgcgtgg tggtagcgt aagccacgaa gaccctgagg      180

tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg     240

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ggctgaatgg caaggagtag aagtgaagg tctccaacaa agccctccca acccccatcg 360  
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420  
catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct 480  
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540  
ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctacagcaag ctcaccgtgg 600  
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660  
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<223> reverse primer useful for generation of a synthetic gamma activation site (GAS) containing promoter element

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aaatatctgc catctcaatt agtcagcaac catagtcccc cccctaactc cgcccatccc 120  
gcccctaact ccgcccagtt ccgcccattc tccgcccatt ggctgactaa ttttttttat 180  
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<213> Artificial Sequence

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<223> NF-KB binding site

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ccatctcaat tag                                                                73

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caattagtcg gcaaccatag tcccgcctct aactccgccc atcccgcctc taactccgcc      120
cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga      180
ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg      240
cttttgcaaa aagctt                                                            256

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**UNITED STATES PATENT AND TRADEMARK OFFICE**  
**CERTIFICATE OF CORRECTION**

PATENT NO. 6,905,688  
APPLICATION NO.: 09/833,118  
ISSUE DATE: June 14, 2005  
INVENTOR(S): Craig A. Rosen et al.

It is hereby certified that an error or errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

In the Title Page

Under item (60) (Related U.S. Application Data) of the title page, delete the text beginning with "Provisional application No. 60/229,358" to and ending "provisional application No. 60/199,384, filed on Apr. 25, 2000."

In the Specification:

Col. 1, line 3, delete the text beginning with "This application" to and ending "in its entirety." in col. 1, line 8.

In the Claims:

Col. 292, lines 36-37, in claim 1(j), delete the text "wherein the brain derived neurotrophic factor protein or fragment thereof,".

Col. 292, line 57, in claim 4, "viva" should read --vivo--.

Col. 294, line 15, in claim 15, delete "any of".

Col. 294, line 17, in claim 16, delete "any of".

In the Sequence Listing:

Delete the Sequence Listing beginning in Col. 263, beginning with the text "<160> NUMBER OF SEQ ID NOS: 35" to and ending "<400> SEQUENCE: 35"

Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu  
1 5 10 15

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Washington, D.C. 20001-4413

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Trp Ala Pro Ala Arg Gly"

20

in Col. 292 and insert the following Sequence Listing:

<160> NUMBER OF SEQ ID NOS: 45

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221> primer\_bind

<223> primer useful to clone human growth hormone cDNA

<400> 1

cccaagaatt cccttatcca ggc

23

<210> 2

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<221> primer\_bind

<223> primer useful to clone human growth hormone cDNA

<400> 2

gggaagctta gaagccacag gatccctcca cag

33

<210> 3

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<221> misc\_structure

<223> synthetic oligonucleotide used to join DNA fragments  
with non-cohesive ends.

<400> 3

gataaagatt cccaac

16

<210> 4

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<221> misc\_structure

<223> synthetic oligonucleotide used to join DNA fragments  
with non-cohesive ends.

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<400> 4  
aattgttggg aatcttt

17

<210> 5  
<211> 17  
<212> DNA  
<213> Artificial Sequence

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<221> misc\_structure  
<223> synthetic oligonucleotide used to join DNA fragments  
with non-cohesive ends.

<400> 5  
ttaggcttat tcccaac

17

<210> 6  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_structure  
<223> synthetic oligonucleotide used to join DNA fragments  
with non-cohesive ends.

<400> 6  
aattgttggg aataagcc

18

<210> 7  
<211> 24  
<212> PRT  
<213> Artificial Sequence

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<221> SITE  
<222> 1)..(19)  
<223> invertase leader sequence

<220>  
<221> SITE  
<222> 20)..(24)  
<223> first 5 amino acids of mature human serum albumin

<400> 7  
Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys  
1 5 10 15

Ile Ser Ala Asp Ala His Lys Ser  
20

<210> 8  
<211> 21

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<212> DNA  
<213> Artificial Sequence

<220>  
<221> misc\_structure  
<223> synthetic oligonucleotide used to join DNA  
fragments with non-cohesive ends.

<400> 8  
gagatgcaca cctgagtgag g

21

<210> 9  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
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<223> synthetic oligonucleotide used to join DNA  
fragments with non-cohesive ends.

<400> 9  
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27

<210> 10  
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<212> DNA  
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<220>  
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<223> synthetic oligonucleotide used to join DNA  
fragments with non-cohesive ends.

<400> 10  
ctcttggtgtg catcgaagcc acag

24

<210> 11  
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<212> DNA  
<213> Artificial Sequence

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<223> synthetic oligonucleotide used to join DNA  
fragments with non-cohesive ends.

<400> 11  
tgtggaagag cctcagaatt tattccaac

30

<210> 12  
<211> 31  
<212> DNA

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<213> Artificial Sequence

<220>

<221> misc\_structure

<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 12

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31

<210> 13

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<221> misc\_structure

<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

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47

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<211> 48

<212> DNA

<213> Artificial Sequence

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<221> misc\_structure

<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

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48

<210> 15

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<221> misc\_structure

<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 15

ttaggcttag gcggtggtgg atctggtggc ggcggatctg gtggcgggtgg atccttccca 60  
ac 62

<210> 16

<211> 63

<212> DNA

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<213> Artificial Sequence

<220>

<221> misc\_structure

<223> synthetic oligonucleotide used to join DNA fragments with non-cohesive ends.

<400> 16

aattgttggg aaggatccac cgccaccaga tccgccgcca ccagatccac caccgcctaa 60  
gcc 63

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<211> 1782

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)..(1755)

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1 5 10 15  
gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag 96  
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln  
20 25 30  
cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144  
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
35 40 45  
ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa 192  
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys  
50 55 60  
tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt 240  
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
65 70 75 80  
cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct 288  
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
85 90 95  
gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc 336  
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu  
100 105 110  
ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat 384  
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
115 120 125  
gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga 432  
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg

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130	135	140	
aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg	480		
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg			
145 150 155 160			
tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc	528		
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala			
165 170 175			
tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg	576		
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser			
180 185 190			
tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa	624		
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu			
195 200 205			
aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc	672		
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro			
210 215 220			
aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa	720		
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys			
225 230 235 240			
gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac	768		
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp			
245 250 255			
agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc	816		
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser			
260 265 270			
agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac	864		
Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His			
275 280 285			
tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca	912		
Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser			
290 295 300			
tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct	960		
Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala			
305 310 315 320			
gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga	1008		
Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg			
325 330 335			
agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca	1056		
Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr			
340 345 350			
tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa	1104		
Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu			
355 360 365			

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tgc tat gcc aaa gtg ttc gat gaa ttt aaa cct ctt gtg gaa gag cct	1152
Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro	
370 375 380	
cag aat tta atc aaa caa aac tgt gag ctt ttt gag cag ctt gga gag	1200
Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu	
385 390 395 400	
tac aaa ttc cag aat gcg cta tta gtt cgt tac acc aag aaa gta ccc	1248
Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro	
405 410 415	
caa gtg tca act cca act ctt gta gag gtc tca aga aac cta gga aaa	1296
Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys	
420 425 430	
gtg ggc agc aaa tgt tgt aaa cat cct gaa gca aaa aga atg ccc tgt	1344
Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys	
435 440 445	
gca gaa gac tat cta tcc gtg gtc ctg aac cag tta tgt gtg ttg cat	1392
Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His	
450 455 460	
gag aaa acg cca gta agt gac aga gtc aca aaa tgc tgc aca gag tcc	1440
Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser	
465 470 475 480	
ttg gtg aac agg cga cca tgc ttt tca gct ctg gaa gtc gat gaa aca	1488
Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr	
485 490 495	
tac gtt ccc aaa gag ttt aat gct gaa aca ttc acc ttc cat gca gat	1536
Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp	
500 505 510	
ata tgc aca ctt tct gag aag gag aga caa atc aag aaa caa act gca	1584
Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala	
515 520 525	
ctt gtt gag ctt gtg aaa cac aag ccc aag gca aca aaa gag caa ctg	1632
Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu	
530 535 540	
aaa gct gtt atg gat gat ttc gca gct ttt gta gag aag tgc tgc aag	1680
Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys	
545 550 555 560	
gct gac gat aag gag acc tgc ttt gcc gag gag ggt aaa aaa ctt gtt	1728
Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val	
565 570 575	
gct gca agt caa gct gcc tta ggc tta taacatctac atttaaaagc atctcag	1782
Ala Ala Ser Gln Ala Ala Leu Gly Leu	
580 585	

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<210> 18  
<211> 585  
<212> PRT  
<213> Homo Sapiens

<400> 18

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu  
1 5 10 15  
Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln  
20 25 30  
Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu  
35 40 45  
Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys  
50 55 60  
Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu  
65 70 75 80  
Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro  
85 90 95  
Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu  
100 105 110  
Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His  
115 120 125  
Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg  
130 135 140  
Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg  
145 150 155 160  
Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala  
165 170 175  
Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser  
180 185 190  
Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu  
195 200 205  
Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro  
210 215 220  
Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys  
225 230 235 240  
Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp  
245 250 255  
Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser  
260 265 270

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Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His  
 275 280 285  
 Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser  
 290 295 300  
 Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala  
 305 310 315 320  
 Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg  
 325 330 335  
 Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr  
 340 345 350  
 Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu  
 355 360 365  
 Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro  
 370 375 380  
 Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu  
 385 390 395 400  
 Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro  
 405 410 415  
 Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys  
 420 425 430  
 Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys  
 435 440 445  
 Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His  
 450 455 460  
 Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser  
 465 470 475 480  
 Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr  
 485 490 495  
 Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp  
 500 505 510  
 Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala  
 515 520 525  
 Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu  
 530 535 540  
 Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys  
 545 550 555 560  
 Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val  
 565 570 575

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Ala Ala Ser Gln Ala Ala Leu Gly Leu  
580 585

<210> 19  
<211> 58  
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<223> primer used to generate XhoI and ClaI  
site in pPPC0006

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<210> 20  
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site in pPPC0006

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<210> 21  
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site in pPPC0006

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site in pPPC0006

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<400> 22  
cacttctcta gagtggtttc atatgtctt

29

<210> 23  
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<212> DNA  
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<220>  
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<210> 24  
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<213> Artificial Sequence

<220>  
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<223> Synthetic oligonucleotide used to alter restriction  
sites in pPPC0007

<400> 24  
agaattaagc ttagtttaaa cggccggccg gcgcgcctta ttataagcct aaggcagctt 60

<210> 25  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> primer\_bind  
<223> forward primer useful for generation of albumin  
fusion protein in which the albumin moiety is N-terminal  
of the Therapeutic Protein

<220>  
<221> misc feature  
<222> (18)  
<223> n equals a,t,g, or c

<220>  
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<220>  
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<223> n equals a,t,g, or c

<220>

<221> misc feature

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MAR 9 2000

<220>  
<221> misc feature  
<222> (32)  
<223> n equals a,t,g, or c

<400> 25  
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32

<210> 26  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
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<223> reverse primer useful for generation of albumin  
fusion protein in which the albumin moiety is N-terminal  
of the Therapeutic Protein

<220>  
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<223> n equals a,t,g, or c

<220>  
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<220>  
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51

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<220>

<223> forward primer useful for generation of albumin fusion protein in which the albumin moiety is c-terminal of the Therapeutic Protein

<220>

<221> misc feature

<222> (19)

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<220>

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<221> misc feature  
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<223> n equals a,t,g, or c

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aggagcgtcg acaaaagann nnnnnnnnnn nnn

33

<210> 28

<211> 52

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52

<210> 29  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<221> signal  
<223> signal peptide of natural human serum albumin protein

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<400> 29  
 Met Lys Trp Val Ser Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala  
     1                    5                    10                    15

Tyr Ser Arg Ser Leu Asp Lys Arg  
                     20

<210> 30  
 <211> 114  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 <223> forward primer useful for generation of PC4:HSA  
 albumin fusion VECTOR

<220>  
 <221> misc\_feature  
 <222> (5)..(10)  
 <223> BamHI restriction site

<220>  
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 <222> (11)..(16)  
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<220>  
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 <222> (17)..(27)  
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<220>  
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 <222> (25)..(97)  
 <223> cds natural signal sequence of human serum albumin

<220>  
 <221> misc\_feature  
 <222> (75)..(81)  
 <223> XhoI restriction site

<220>  
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 <222> (98)..(114)  
 <223> cds first six amino acids of human serum albumin

<400> 30  
 tcagggatcc aagcttcgc caccatgaag tgggtaacct ttatttcct tctttttctc 60  
 tttagctcgg cttactcgag ggggtgtgtt cgtcgagatg cacacaagag tgag 114

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 <213> Artificial Sequence

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```

<220>
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<223> reverse primer useful for generation of
PC4:HSA albumin fusion VECTOR

<220>
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<220>
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<222> (12)..(17)
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<220>
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<222> (15)..(17)
<223> reverse complement of stop codon

<220>
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<222> (18)..(25)
<223> AscI restriction site

<220>
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<222> (18)..(43)
<223> reverse complement of DNA sequence encoding last 9 amino acids

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gcagcggtac cgaattcggc ggccttata agcctaaggc agc
43

<210> 32
<211> 46
<212> DNA
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<220>
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<223> forward primer useful for inserting Therapeutic
protein into pC4:HSA vector

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ccgccgctcg aggggtgtgt ttctcgann nnnnnnnnnn nnnnnn

46

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<211> 55  
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<220>  
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protein into pC4:HSA vector

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<223> n equals a,t,g, or c

<220>

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<222> (43)

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<222> (45)

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<211> 17
<212> PRT
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<221> signal
<223> Stanniocalcin signal peptide

<400> 34
Met Leu Gln Asn Ser Ala Val Leu Leu Leu Leu Val Ile Ser Ala Ser
  1              5              10              15

Ala

<210> 35
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> signal
<223> Synthetic signal peptide

<400> 35
Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Ala Leu
  1              5              10              15

Trp Ala Pro Ala Arg Gly
              20

<210> 36
<211> 733
<212> DNA
<213> Homo sapiens

<400> 36
gggatccgga gcccaaatct tctgacaaaa ctacacatg cccaccgtgc ccagcacctg      60

aattcgaggg tgcaccgtca gtcttctct tcccccaaa acccaaggac accctcatga      120

tctcccgga tcttgaggtc acatgcgtgg tggtagcgt aagccacgaa gacctgagg      180

tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg      240

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aggagcagta caacagcacg tacgtgtgg tcagcgtcct caccgtcctg caccaggact 300
ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg 360
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct 480
atccaagcga catgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540
ccacgcctcc cgtgctggac tccgacggct ctttcttct ctacagcaag ctaccgtgg 600
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggtctctg 660
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gactctagag gat 733

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<211> 5
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<220>
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<400> 37
Trp Ser Xaa Trp Ser
1 5

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<210> 38
<211> 86
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<213> Artificial Sequence

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<221> primer_bind
<223> forward primer useful for generation of a synthetic gamma activation site
(GAS) containing promoter element

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<400> 38
gcgcctcgag atttccccga aatctagatt tccccgaaat gatttccccg aatgatttc 60
cccgaatat ctgccatctc aattag 86

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<210> 39
<211> 27
<212> DNA

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<213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <223> reverse primer useful for generation of a synthetic gamma activation site  
 (GAS) containing promoter element

<400> 39  
 gcggcaagct ttttgcaaag cctaggc 27

<210> 40  
 <211> 271  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> misc\_feature  
 <223> Synthetic GAS-SV40 promoter sequence

<400> 40  
 ctcgagatTT ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg 60  
 aaatatctgc catctcaatt agtcagcaac catagtcccc ccctaactc cgcccatccc 120  
 gccctaact cgcgccagtt cgcgccattc tccgccccat ggctgactaa ttttttttat 180  
 ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240  
 ttttgaggc ctaggctttt gcaaaaagct t 271

<210> 41  
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 <212> DNA  
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 <223> primer useful for generation of a EGR/SEAP reporter construct

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 gcgctcgagg gatgacagcg atagaacccc gg 32

<210> 42  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 <223> primer useful for generation of a EGR/SEAP reporter construct

<400> 42  
 gcgaagcttc gcgactcccc ggatccgcct c 31

<210> 43  
 <211> 12  
 <212> DNA

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<213> Artificial Sequence

<220>
<221> misc_binding
<223> NF-KB binding site

<400> 43
ggggactttc cc                                     12

<210> 44
<211> 73
<212> DNA
<213> Artificial Sequence

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<221> primer_bind
<223> forward primer useful for generation of a vector containing the NF-KB
promoter element

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gcggcctcga ggggactttc ccggggactt tccggggact ttccgggact ttccatcctg      60
ccatctcaat tag                                                                73

<210> 45
<211> 256
<212> DNA
<213> Artificial Sequence

<220>
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<223> Synthetic NF-KB/SV40 promoter

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ctcgagggga ctttcccgga gactttccgg ggactttccg ggactttcca tctgccatct      60
caattagtcg gcaaccatag tcccgcacct aactccgccc atccgcgccc taactccgcc      120
cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga      180
ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg      240
cttttgcaaa aagctt                                                                256

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